SEQUENCE LISTING

<110> Parham, Chrisler L.
       Moore, Kevin W.
       Murgolo, Nicholas J.
       Bazan, J. Fernando

<120> Human Receptor Proteins; Related Reagents and Methods

<130> DX0804K

<140> 09/265,540
<141> 1999-03-08

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<170> PatentIn Ver. 2.0

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gaagcaacca tcagaggcag ggtggtttgt ckaacagaac aaytgactga ggytakrggg  1264

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Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val
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Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu Tyr Thr Ser
65                  70                  75                  80

His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu
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Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg
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Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys
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Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu Pro Gly Ala
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Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu
        180                 185                 190

Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe
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Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val
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Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe
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Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp Lys
            245                 250                 255

Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val Leu Pro
            260                 265                 270

Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Arg
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Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile
           20                  25                  30

tgg gtg acg ccg gga gaa gcc tcc ctc atc atc agg ttc tcc tct ccc   145

Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
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           50                  55                  60

tgg gaa aag gcg gga atc caa aag gtt aaa ggt cct ttc aag agc aac   241

Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn
 65              70                  75                  80

tcc atc gtg ttg gat ggc ttg aga ccc tta aga gaa tac tgt tta caa   289

Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
                85                  90                  95

gtg aag gcg cat ctc ttt cgc aca tcc tgc aac acc tct agg ccc ggc   337

Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
           100                 105                 110

cgc tta agc aac ata act tgc tac gaa aca atg atg gat gcc act acg   385

Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
           115                 120                 125

aag ctt caa caa gtc atc ctc atc gcc gtg gga gtc ttt ctg tcg ctg   433

Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
           130                 135                 140

gcg gcg ctg gcg ggg ggc tgt ttc ttc ctg gtg ctg aga tac aaa ggc   481

Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly
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gaa gag tat ctg aag gac ccg agc cag cct atc cta gag gcc ctg gac    577
Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp
                180                 185                 190

aag gac acg tca cca aca gat gat gcc tgg gac ttg gtg tct gtt gtt    625
Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val
                195                 200                 205

gca ttt cca gca aag gag caa gaa gat gtt ccc caa agc act ttg acc    673
Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr
    210                 215                 220

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Gln Asn Ser Gly Ala Val Cys
225                 230

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Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa
        50              55              60

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65              70              75              80

Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
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Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
            100             105             110

Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
        115             120             125

Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
        130             135             140

Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly
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Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile
            165             170             175

Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp
            180             185             190

Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val
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Gln Asn Ser Gly Ala Val Cys
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Val Gln Phe Lys Tyr Thr Asp Ser Lys Trp Phe Thr Ala Asp Ile Met
65   70   75   80

Ser Ile Gly Val Asn Cys Thr Gln Ile Thr Ala Thr Glu Cys Asp Phe
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Thr Ala Ala Ser Pro Ser Ala Gly Phe Pro Met Asp Phe Asn Val Thr
            100   105   110

Leu Arg Leu Arg Ala Glu Leu Gly Ala Leu His Ser Ala Trp Val Thr
            115   120   125

Met Pro Trp Phe Gln His Tyr Arg Asn Val Thr Val Gly Pro Pro Glu
    130   135   140

Asn Ile Glu Val Thr Pro Gly Glu Gly Ser Leu Ile Ile Arg Phe Ser
145   150   155   160

Ser Pro Phe Asp Ile Ala Asp Thr Ser Thr Ala Phe Phe Cys Tyr Tyr
            165   170   175

Val His Tyr Trp Glu Lys Gly Gly Ile Gln Gln Val Lys Gly Pro Phe
            180   185   190

Arg Ser Asn Ser Ile Ser Leu Asp Asn Leu Lys Pro Ser Arg Val Tyr
    195   200   205

Cys Leu Gln Val Gln Ala Gln Leu Leu Trp Asn Lys Ser Asn Ile Phe
    210   215   220

Arg Val Gly His Leu Ser Asn Ile Ser Cys Tyr Glu Thr Met Ala Asp
225   230   235   240

Ala Ser Thr Glu Leu Gln Gln Val Ile Leu Ile Ser Val Gly Thr Phe
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Tyr Arg Gly Leu Ile Lys Tyr Trp Phe His Thr Pro Pro Ser Ile Pro
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Leu Gln Ile Glu Glu Tyr Leu Lys Asp Pro Thr Gln Pro Ile Leu Glu
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Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
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Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
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Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
            85   90   95

His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
            100   105   110

Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His
        115   120   125

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Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
145             150             155             160

Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
            165             170             175

Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
            180             185             190

Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
        195             200             205

Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Trp Met Val Ala
210             215             220

Val Ile Leu Met Ala Ser Val Phe Met Val Cys Leu Ala Leu Leu Gly
225             230             235             240

Cys Phe Ser Leu Leu Trp Cys Val Tyr Lys Lys Thr Lys Tyr Ala Phe
            245             250             255

Ser Pro Arg Asn Ser Leu Pro Gln His Leu Lys Glu Phe Leu Gly His
            260             265             270

Pro His His Asn Thr Leu Leu Phe Phe Ser Phe Pro Leu Ser Asp Glu
        275             280             285

Asn Asp Val Phe Asp Lys Leu Ser Val Ile Ala Glu Asp Ser Glu Ser
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Gly Lys Gln Asn Pro Gly Asp Ser Cys Ser Leu Gly Thr Pro Pro Gly
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BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

RECEIVED

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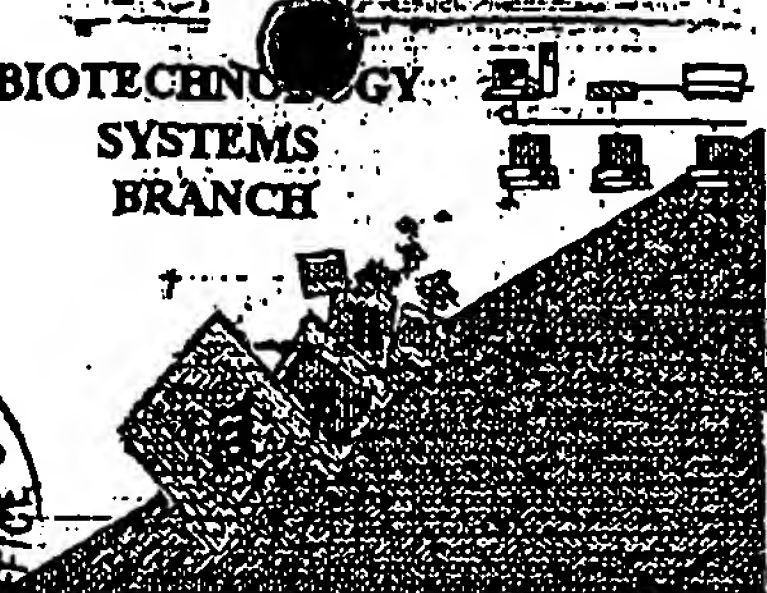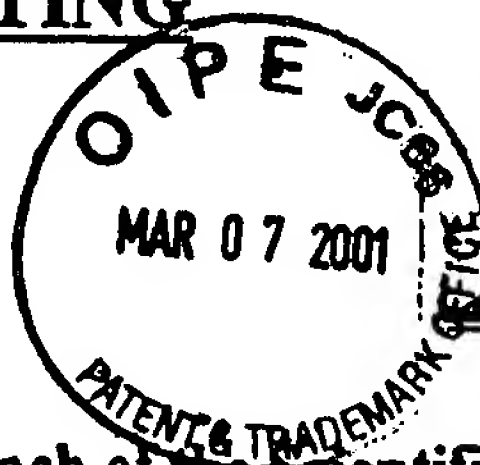
JAN 1 0 2001

The Biotechnology Systems Branch of the Scientific and Technical Information TECH CENTER
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _09/265,540C_

Source: _1643_

Date Processed by STIC: _1/2/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
 PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
 PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0
The Checker Version 3.0 application is a state-of the-art Windows based software program
employing a logical and intuitive user-interface to check whether a sequence listing is in
compliance with format and content rules. Checker Version 3.0 works for sequence listings
generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old
rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual
Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-
compliant. Checker allows public users to check sequence listings in Computer Readable form
(CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence
listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
 http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u> <u>SUGGESTED CORRECTION</u> SERIAL NUMBER: 09/265,540C

RECEIVED

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos   The amino acid number/text at the end of each line "wrapped " down to the next line.   **JAN 10 2001**
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

TECH CENTER

3 _____ Incorrect Line Length   The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid   The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering   between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII   This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES)   <210> sequence id number
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10 _____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES)   Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism   Sequence(s) _____ are missing this mandatory field or its response.
(NEW RULES)

12 _____ Use of <220>Feature   Sequence(s) _____ are missing the <220>Feature and associated headings.
(NEW RULES)   Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

RAW SEQUENCE LISTING   DATE: 01/01/2001
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 1          Moore, Kevin W
 5          Burgato, Nicholas J.
 6          Bazan, J. Fernando
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10 <130> FILE REFERENCE: DX0901K
12 <140> CURRENT APPLICATION NUMBER: 09/265,540C
14 <141> CURRENT FILING DATE: 1999-03-08
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30 <222> LOCATION: (567)
31 <223> OTHER INFORMATION: n at position 567; n may be A, C, G, or T;
32          translated amino acid depends on genetic code
34 <220> FEATURE:
35 <221> NAME/KEY: misc_feature
36 <222> LOCATION: (573)
37 <223> OTHER INFORMATION: n at position 573; n may be A, C, G, or T;
38          translated amino acid depends on genetic code
40 <220> FEATURE:
41 <221> NAME/KEY: misc_feature
42 <222> LOCATION: (1136)
43 <223> OTHER INFORMATION: n at position 1136; n may be A,C, G, or T;
44          translated amino acid depends on genetic code
46 <220> FEATURE:
47 <221> NAME/KEY: misc_feature
48 <222> LOCATION: (1142)
49 <223> OTHER INFORMATION: n at position 1142; n may be A, C, G, or T;
50          translated amino acid depends on genetic code
52 <220> FEATURE:
53 <221> NAME/KEY: misc_feature
54 <222> LOCATION: (1169)
55 <223> OTHER INFORMATION: n at position 1169; n may be A, C, G, or T;
56          translated amino acid depends on genetic code
58 <400> SEQUENCE: 1
59 tcaccccca cgtccgcgct gcaactcaga cctcagctcc aacatatgca ttctgaagaa   60
61 agatcgtctga gatggaccga atcgctctct ttggcaagaa acaatgttct cgttcaaact  120
63 gagtctacca n atg gag act ttc acc atg gtg cta gag cag ata tgg aca  170
64                Met Glu Thr Phe Thr Met Val Leu Glu Gln Ile Trp Thr
```

02/22/01 THU 00:40 FAX 703 308 0294   GF 1600 FAX MACHINE 7   005

RAW SEQUENCE LISTING   DATE: 01/02/2001
PATENT APPLICATION: US/09/265,540C   TIME: 12:53:11

    Input Set : A:\804k.app
    Output Set : N:\CRF3\01022001\1265540C.raw

```
65
67  agt ctt tte atg tgg ttt ttc tac gca ttg att cca tgt ctg ctc aca      218
68  Ser Leu Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr
69       15              20              25
71  gat gta gtg gcc att ctg cct gcc cct cag aac ctc tct gta ctc tca      266
72  Asp Gln Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
73       30              35              40              45
75  acc aac atg aag cat ctc ttg atg tgg agc cca gtg atc gca cct gga      311
76  Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly
77       50              55              60
79  gaa aca gtg tac tat tgt gtc gaa tac cag ggg aat tac cag agc ttg      ?
80  Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Gln Ser Leu
81       65              70              75
83  tac acg agc cac atc tgg atc ccc agc agc tgg tgc tct ctc acc gaa      ?
84  Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu
85       80              85              90
87  ggt cct gag tgt gat gtc act gat gac ata agg gcc act gtg cca tac      ?
88  Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr
89       95              100             105
91  aac ctt aca gtc agg gcc aca ttg ggc tca cag ttc tca gct tgg agc      500
92  Asn Leu Thr Val Arg Ala Thr Leu Gly Ser Gln Phe Ser Ala Trp Ser
93  110             115             120             125
95  atc ctg aag cat ccc ttt gat aga aac ttc atc atc ctt acc caa cct      554
96  Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Ala Pro
97  130             135             140
99  ggg atg gag atc ggc aaa gse ggc ttc cac ctg gtt att gag ctg gag      602
100 Gly Met Glu Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Gln
101 145             150             155
103 gac ctg ggg ccc cag ttt gag ttc ctc gtg gcc tac tgg aga gag      650
104 Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu
105 160             165             170
107 cct ggt gcc gag gaa cat gtc aaa aca gtg agg agt ggt att cca      698
108 Pro Gly Ala Glu Glu His Val Lys Thr Val Arg Ser Gly Gly Ile Pro
109 175             180             185
111 gtg cac cta gaa acc atg gaa cca gga gct gca tac tgt gtg aaa gcc      746
112 Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala
113 190             195             200             205
115 cag aca ttc gtg aag gcc att ggg acg tac agc gcc ttc agc cag aca      794
116 Gln Thr Phe Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr
117 210             215             220
119 gaa tgt gtg gat gtg caa gga gag gcc att ccc ctg gta ctg gcc ctg      842
120 Glu Cys Val Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu
121 225             230             235
123 ttt gcc ttc gtt ggc ttc atg ctg atc ctg gtc gtg cca ctg ttc      890
124 Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe
125 240             245             250
127 gtc tgg aaa atg ggc cgg ctg ctc cag tac tcc tgt tgc ccc gtg gtg      938
128 Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val
129 255             260             265
```

Please align amino acids directly under corresponding codon.

FEB 22 '01 03:50   703 308 0294   PAGE 05

RAW SEQUENCE LISTING   DATE: 01/0../200?
PATENT APPLICATION: US/09/265,540C   TIME: 12:55:11

Input Set. : A:\804K.app
Output Set: N:\CRF3\01022001\I265540C.raw

```
141 gtc ctc cca gac acc ttg gaa ata aar gat ctc cac caq aat ctc atc  986
132 Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile
133 270          275          280          285
135 agc tgc aga cgg gag gag gtg gat gcc tgt gcc act gct gtg atg tct  1031
136 Ser Cys Arg Arg Glu Gln Val Asp Ala Cys Ala Thr Ala Val Met Ser
137          290          295          300
139 cct gag gaa ctc ctc agg gcc tgg atc tca tagcttcca gaggcccca  1084
140 Pro Gln Glu Leu Leu Arg Ala Trp Ile Ser
141          305          310
143 agtaaagccg agaacctgat ctgcatgaca ttgaaccccat gaaagaacaa gctgtgttcc  1141
145 tgttttcacga cacggacaaa gaatgagaaa actagaatga ggctcttgtc tacaagtctca  1201
147 gagcaaacca tcagaggcag agtggtttat ckaacctcac agctctctgt gactacctt  1261
149 cctgtgacct cctggcckja qgstkscant tgcwtgqytg mcaagtcctg qqaaaagtga  1321
151 cttcatcccn tnggtccnnn gtttctctct ctgtaatggg ggatncctac aaaactg  1381
153 <210> SEQ ID NO: 2
155 <211> LENGTH: 311
156 <212> TYPE: PRT
157 <213> ORGANISM: primate
159 <400> SEQUENCE: 2
160 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu Phe
161 1          5          10          15
163 Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp Gln Val
164          20          25          30
166 Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser Thr Asn Met
167          35          40          45
169 Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val
170          50          55          60
172 Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Gln Ser Leu Tyr Thr Ser
173 65          70          75          80
175 His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Gln Gly Pro Gln
176          85          90          95
178 Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Leu Tyr Asn Leu Arg
179          100          105          110
181 Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys
182          115          120          125
184 His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu
185          130          135          140
187 Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly
188 145          150          155          160
190 Pro Gln Phe Glu Thr Leu Val Ala Tyr Trp Xaa Arg Glu Pro Gly Ala
191          165          170          175
193 Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu
194          180          185          190
196 Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe
197          195          200          205
199 Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val
200          210          215          220
202 Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe
203          225          230          235          240
```

see item 10 on Error Summary Sheet

```
205 Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp Lys
206              245                 250                 255
208 Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val Leu Pro
209              260                 265                 270
211 Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Asn
212         275                 280                 285
214 Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser Pro Glu Glu
215         290                 295                 300
217 Leu Leu Arg Ala Trp Ile Ser
218 302                 316
221 <210> SEQ ID NO. 4
222 <211> LENGTH: 1244
223 <212> TYPE: DNA
224 <213> ORGANISM: primate
226 <220> FEATURE:
227 <221> NAME/KEY: CDS
228 <222> LOCATION: (2)..(694)
230 <400> SEQUENCE: 4
231 c cgg gtc gac cca cgc gtc cgg gtt tcc acc tgg ctg aca gtg cct  49
232   Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro
233   1               5                 10                15
235 tgg atc ctg ctc tgt tgg aat gtc acc att ggg cct cct cag agc atc  97
236 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Gln Ser Ile
237             20                  25                  30
239 tgg gtg acc cca gga gaa gcc tcc ctc atc atc aga ttc tcc tct cca  145
240 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
241             35                  40                  45
243 ttc gac gtc cct cca aac ctg ggc tat ttc cag tac tat gtc cat gag  193
244 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa
245         50                  55                  60
247 tgg cag aag gcg gga atc caa aag gtt aaa ggt cct ttc aag agc aac  241
248 Trp Gln Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn
249 65                  70                  75                  80
251 tcc atc gtg ctt gat ggc ttg aga ccc tta aga gaa tac tgt cta caa  289
252 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
253             85                  90                  95
255 gtg aag gcg cat ctc ttt cgc aca tcc tgc aac acc tct agu cct ggc  337
256 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
257             100                 105                 110
259 cgc tta agc aaa ata act tgc tac gaa aca atg atg gat gcc act acg  385
260 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
261             115                 120                 125
263 aag ctc caa caa gtc atc ctc atc gcc gta gga gtc ctt ctg ctg ctg  433
264 Lys Leu Glu Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
265     130                 135                 140
267 gca gcg ctg gca ggg ggc tgt ttc ttc ctg gtg ctg aga tac aaa ggc  481
268 Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly
269 145                 150                 155                 160
271 ctg gtg aaa tac tgg ttt cac tct cag gaa agc atc caa ttg cag atc  529
```

RAW SEQUENCE LISTING   DATE: 01/02/2001
PATENT APPLICATION: US/09/265,540C   TIME: 12:00:00

Input Set : A:\804k.app
Output Set: N:\CRF3\01022001\I265540C.raw

```
272  Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile
273              165              170              175
275  gca gag tat ctg aag gac cct agc cag ccc atc ctg gaa gca ctg gac   577
276  Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp
277              180              185              190
279  aag gac agg tca cca aca gat gat gca tgg gac ttg agg tct gtt gtt   625
280  Lys Asp Ser Pro Thr Asp Asp Ala Trp Asp Leu Arg Ser Val Val
281              195              200              205
283  gca ttt cca gca aag gaa caa gaa gat gtt cca cag agc act ctg acc   673
284  Ala Phe Pro Ala Lys Gln Gln Glu Asp Val Pro Gln Ser Thr Leu Thr
285              210              215              220
287  cag aac tct ggt gct gtc tgc tgacctgtag gttgggggct ctgggccag     721
288  Gln Asn Ser Gly Ala Val Cys
289  225                   230
291  gaacatgata atgtcctgt caggactcta tggaatccag tcctgctcct tcctgtccca  781
293  aaagagcccg tcatcacctg tgaaaatgta taggaacgag tagaagcaac gaacttattg  841
295  atttttcttct tcaaactaag agtttctaga caatacgcgt ttttagaata tttctaacaa  901
297  tatgtccccg aaagattagg atttctcctta gacaatgag agacagtgtc ttatttgtta  961
299  gcaaatcgtgc gtccgacct cctctgaaac ttttcagtca gcagcaaga ccgagaatcc 1021
301  ctctcttgat gaagccctc agtgagccaa tatcacctat ctcagcctge ctccaagaaga 1081
303  gacattagat gtccctccct catatccaac caaccgaacc gacatgtgat tagaactgta 1141
305  aatcagatca gtaggattaa gcctttttt ctgtccagtt aggaataaaca gactctactc 1201
307  aacttttaa aagaagataat aaaaaaaaaa aaaaatcaac                        1244
310  <210> SEQ ID NO: 4
311  <211> LENGTH: 231
312  <212> TYPE: PRT
313  <213> ORGANISM: primate
315  <400> SEQUENCE: 4
316  Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro
317  1                5              10              15
319  Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile
320              20              25              30
322  Trp Val Thr Pro Gly Gln Ala Ser Leu Ile Ile Arg Phe Ser Ser Ser
323              35              40              45
```
W--> 325 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His (Xaa) item 10
```
326              50              55              60
328  Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Leu Ser Asn
329  65              70              75              80
331  Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Trp Cys Leu Gln
332              85              90              95
334  Val Cys Ala His Leu Phe Arg Thr Ser Asn Thr Ser Arg Pro Gly
335              100              105              110
337  Arg Leu Ser Asn Ile Phe Cys Tyr Glu Thr Met Ser Asp Ala Thr Thr
338              115              120              125
340  Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
341              130              135              140
343  Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly
344  145              150              155              160
346  Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile
```

```
VERIFICATION SUMMARY                    DATE: 01/0../2001
PATENT APPLICATION:  US/09/265,540C     TIME: 13:5..:..

Input Set  : A:\804K.app
Output Set : N:\CRF3\01022001\I265540C.raw

L:99  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:100 M:441 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:104 M:341 W: (46) " " or "Xaa" used, for SEQ ID#:1
L:116 M:441 W: (16) " " or "Xaa" used, for SEQ ID#:1
L:120 M:441 W: (16) "n" or "Xaa" used, for SEQ ID#:1
L:151 M:441 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:15. M:258 W: Mandatory Feature missing, .220. not found for SEQ ID#:3
L:18. M:258 W: Mandatory Feature missing, .221. not found for SEQ ID#:3
L:18. M:258 W: Mandatory Feature missing, .222. not found for SEQ ID#:3
L:18. M:258 W: Mandatory Feature missing, .223. not found for SEQ ID#:3
L:18. M:340 W: (16) "n" or "Xaa" used: feature required, for SEQ ID#:2
L:190 M 258 W: Mandatory Feature missing, .220. not found for SEQ ID#:2
L:190 M:258 W: Mandatory Feature missing, .221. not found for SEQ ID#:2
L:190 M:258 W: Mandatory Feature missing, .222. not found for SEQ ID#:2
L:190 M:258 W: Mandatory Feature missing, .223. not found for SEQ ID#:2
M:140 Repeated in SeqNo#2
L:199 M:258 W: Mandatory Feature missing, .220. not found for SEQ ID#:2
L:199 M:258 W: Mandatory Feature missing, .221. not found for SEQ ID#:2
L:199 M:258 W: Mandatory Feature missing, .222. not found for SEQ ID#:2
L:199 M:258 W: Mandatory Feature missing, .223. not found for SEQ ID#:2
L:202 M:258 W: Mandatory Feature missing, .220. not found for SEQ ID#:2
L:202 M:258 W: Mandatory Feature missing, .221. not found for SEQ ID#:2
L:202 M:258 W: Mandatory Feature missing, .222. not found for SEQ ID#:2
L:202 M:258 W: Mandatory Feature missing, .223. not found for SEQ ID#:2
L:204 M:258 W: Mandatory Feature missing, .223. not found for SEQ ID#:2
L:214 M:340 W: (46) "n" or "Xaa" used: feature required, for SEQ ID#:3
L:225 M:258 W: Mandatory Feature missing, .220. not found for SEQ ID#:4
L:225 M:258 W: Mandatory Feature missing, .221. not found for SEQ ID#:4
L:225 M:258 W: Mandatory Feature missing, .222. not found for SEQ ID#:4
L:225 M:258 W: Mandatory Feature missing, .223. not found for SEQ ID#:4
L:225 M:340 W: (46) "n" or "Xaa" used: feature required, for SEQ ID#:1
```